

From: Gibbs, Terra
Sent: Monday, January 06, 2003 10:50 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request...

) Could you please a regular search SEQ ID NO. 3

of Serial No. 10003354?

2) Also, please do an oligomer search of SEQ ID NO:3. Please limit the hits to 100 nucleotides or less.

Terra Gibbs #79523
AU 1635
Mailbox 11E12
306-3221

THANK YOU!

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: BOB
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 1-13-03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 02:33:22 ; Search time 119 Seconds
(without alignments)
9568.830 Million cell updates/sec

Title: US-10-003-354-3
Perfect score: 3713
Sequence: 1 attaacagcggtgtagg.....aaacttaagagttatta 3713

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	17	0.5	42	4	US-09-171-425-2
c 2	17	0.5	48	4	Sequence 2, Appli
c 3	17	0.5	48	4	Sequence 6, Appli
4	17	0.5	54	1	US-09-171-425-7
5	17	0.5	54	1	Sequence 7, Appli
6	16	0.4	49	6	Sequence 1044, Ap
7	16	0.4	47	4	Sequence 1044, Ap
c 8	16	0.4	97	1	Patent No. 5516641
c 9	16	0.4	97	1	Sequence 84, Appl
c 10	16	0.4	97	4	Sequence 84, Appl
c 11	16	0.4	97	5	Sequence 57, Appl
12	15	0.4	18	2	Sequence 57, Appl
13	15	0.4	18	3	Sequence 48, Appl
14	15	0.4	18	3	Sequence 64, Appl
15	15	0.4	18	4	Sequence 64, Appl
16	15	0.4	19	2	Sequence 64, Appl
17	15	0.4	19	4	Sequence 3, Appli
18	15	0.4	21	3	Sequence 3, Appli
c 19	15	0.4	21	3	Sequence 23, Appl
20	15	0.4	22	1	Sequence 33, Appl
21	15	0.4	22	4	Sequence 64, Appl
22	15	0.4	22	5	Sequence 64, Appl
23	15	0.4	32	4	Sequence 272, App
24	15	0.4	36	1	Sequence 272, App
25	15	0.4	36	3	Sequence 8, Appli
26	15	0.4	36	4	Sequence 424, App
c 27	15	0.4	44	2	Sequence 5, Appli
					Sequence 59, Appl

28	15	0.4	45	1	US-08-171-389-257	Sequence 257, App
29	15	0.4	45	1	US-08-123-936-257	Sequence 257, App
30	15	0.4	45	2	US-08-475-228A-257	Sequence 257, App
31	15	0.4	45	3	US-08-482-080A-257	Sequence 257, App
32	15	0.4	45	4	US-09-354-947-257	Sequence 257, App
33	15	0.4	45	5	PCT-US93-12388-257	Sequence 257, App
34	15	0.4	46	1	US-08-171-389-102	Sequence 102, App
35	15	0.4	46	1	US-08-123-936-102	Sequence 102, App
36	15	0.4	46	2	US-08-475-228A-102	Sequence 102, App
37	15	0.4	46	3	US-08-482-080A-102	Sequence 102, App
38	15	0.4	46	4	US-09-354-947-102	Sequence 102, App
39	15	0.4	46	5	PCT-US93-12388-102	Sequence 102, App
40	15	0.4	47	4	US-09-641-638-985	Sequence 985, App
c 41	15	0.4	56	4	US-09-390-867A-45	Sequence 45, Appl
c 42	15	0.4	56	4	US-09-390-867A-45	Sequence 45, Appl
c 43	15	0.4	56	4	US-09-548-260-45	Sequence 45, Appl
c 44	15	0.4	56	4	US-09-548-260-46	Sequence 46, Appl
45	15	0.4	74	3	US-08-812-121-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-171-425-2/c
; Sequence 2, Application US/09171425A
; Patent No. 6465438
; GENERAL INFORMATION:
; APPLICANT: Schorr, Joachim
; APPLICANT: Baker, Henry J.
; APPLICANT: Smith, Bruce F.
; TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
; FILE REFERENCE: 08909/003001
; CURRENT APPLICATION NUMBER: US/09/171,425A
; CURRENT FILING DATE: 1998-10-19
; EARLIER APPLICATION NUMBER: PCT/EP97/01943
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotides
US-09-171-425-2

Query Match	0.5%	Score 17:	DB 4:	Length 42;
Best Local Similarity	100.0%	Pred. No. 1.3e+02;		
Matches 17:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2562	CCAGCTTCTTCTTCTTCTT	2578	
Db	41	CCAGCTTCTTCTTCTTCTT	25	

RESULT 2
US-09-171-425-6/c
; Sequence 6, Application US/09171425A
; Patent No. 6465438
; GENERAL INFORMATION:
; APPLICANT: Schorr, Joachim
; APPLICANT: Baker, Henry J.
; APPLICANT: Smith, Bruce F.
; TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
; FILE REFERENCE: 08909/003001
; CURRENT APPLICATION NUMBER: US/09/171,425A
; CURRENT FILING DATE: 1998-10-19
; EARLIER APPLICATION NUMBER: PCT/EP97/01943
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6

; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotides
US-09-171-425-6

Query Match 0.5%; Score 17; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2562 CCAGCTTCTCTCTCTT 2578
|||||

Db 47 CCAGCTTCTCTCTCTT 31

RESULT 3
US-09-171-425-7
; Sequence 7, Application US/09171425A
; Patent No. 6465438
; GENERAL INFORMATION:
; APPLICANT: Schorr, Joachim
; APPLICANT: Baker, Henry J.
; APPLICANT: Smith, Bruce F.
; TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
; FILE REFERENCE: 08909/003001
; CURRENT APPLICATION NUMBER: US/09/171,425A
; CURRENT FILING DATE: 1998-10-19
; EARLIER APPLICATION NUMBER: PCT/EP97/01943
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotides
US-09-171-425-7

Query Match 0.5%; Score 17; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2562 CCAGCTTCTCTCTCTT 2578
|||||

Db 6 CCAGCTTCTCTCTT 22

RESULT 4
US-08-390-850-1044
; Sequence 1044, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,850
FILING DATE: February 17, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/354,920
FILING DATE: December 13, 1994
APPLICATION NUMBER: 08/152,487
FILING DATE: No. 5612215ember 12, 1993
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1044:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-390-850-1044

Query Match 0.5%; Score 17; DB 1; Length 54;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3286 TCAGGGGAAGAGGGGG 3302
:|||||

Db 1 UCAGGGGAAGAGGGGG 17

RESULT 5
US-08-435-634-1044
; Sequence 1044, Application US/08435634
; Patent No. 5731295
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920

;; FILING DATE: December 13, 1994
;; APPLICATION NUMBER: 08/152,487
;; FILING DATE: No. 5731295ember 12, 1993
;; APPLICATION NUMBER: 07/989,848
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 211/084
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1044:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 54 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-435-634-1044

Query Match 0.4%; Score 17; DB 1; Length 54;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3286 TCAGGGGAAGAGGGGG 3302
Db 1 UCAGGGGAAGAAGGGGG 17
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RESULT 6
5516641-1
;; Patent No. 5516641
;; APPLICANT: ULLMAN, EDWIN F.; GOODMAN, THOMAS C.;
;; STULL, PAUL D.
;; TITLE OF INVENTION: METHOD FOR DETECTION OF SPECIFIC
;; NUCLEIC ACID SEQUENCES
;; NUMBER OF SEQUENCES: 4
;; CURRENT APPLICATION DATA:
;; FILING DATE: 10-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 200,373
;; FILING DATE: 18-FEB-1994
;; APPLICATION NUMBER: 993,156
;; FILING DATE: 18-DEC-1992
;; APPLICATION NUMBER: 236,967
;; FILING DATE: 25-AUG-1988
;; SEQ ID NO: 1:
;; LENGTH: 49
5516641-1

Query Match 0.4%; Score 16; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2571 TTCTCTCTTTTCTTTT 2586
Db 22 TTCTCTCTTTTCTTTT 37
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RESULT 7
US-09-364-543-84
;; Sequence 84, Application US/09364543B
;; Patent No. 6331394
;; GENERAL INFORMATION:
;; APPLICANT: Ruckman, Judy
;; APPLICANT: Gold, Larry
;; APPLICANT: Stephens, Andrew
;; APPLICANT: Janjic, Nebojsa
;; TITLE OF INVENTION: Nucleic Acid Ligands to Integrins
;; FILE REFERENCE: NEX82
;; CURRENT APPLICATION NUMBER: US/09/364,543B

;; CURRENT FILING DATE: 1999-07-29
;; NUMBER OF SEQ ID NOS: 118
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 84
;; LENGTH: 87
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Sequence
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (1)...(87)
;; OTHER INFORMATION: All pyrimidines are 2' F.
US-09-364-543-84

Query Match 0.4%; Score 16; DB 4; Length 87;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3350 ATCCACCCCTGCTTG 3365
Db 23 AUCCACCCUGCCUUG 38
:|||||

RESULT 8
US-08-182-175A-48/c
;; Sequence 48, Application US/08182175A
;; Patent No. 5559223
;; GENERAL INFORMATION:
;; APPLICANT: Saverio Carl Falco
;; APPLICANT: Sharon J. Keeler
;; APPLICANT: Janet A. Rice
;; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin
;; NUMBER OF SEQUENCES: 113
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: E.I. du Pont de Nemours and Company
;; STREET: 1007 Market Street
;; CITY: Wilmington
;; STATE: Delaware
;; COUNTRY: USA
;; ZIP: 19898
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy Disk
;; COMPUTER: Macintosh
;; OPERATING SYSTEM: Macintosh System, 6.0
;; SOFTWARE: Microsoft Word, 4.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/182,175A
;; FILING DATE:
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/743,006
;; FILING DATE: 9 August 1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Linda Axamethy Floyd
;; REGISTRATION NUMBER: 33,692
;; REFERENCE/DOCKET NUMBER: BB-1031
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (302) 992-4929
;; TELEFAX: (302) 892-7949
;; TELEX: 835420
;; INFORMATION FOR SEQ ID NO: 48:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 97 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; STRAIN: E. coli
;; CELL TYPE: DH5 alpha
;; IMMEDIATE SOURCE:

; CLONE: 86-H23
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..88
; OTHER INFORMATION: /function= "synthetic storage protein"
; OTHER INFORMATION: /product= "protein"
; OTHER INFORMATION: /gene= "ssp"
; OTHER INFORMATION: /standard_name= "5.8.8.5"
; US-08-182-175A-48

Query Match 0.4%; Score 16; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 CTCCTCCATCTTCTTC 2202
Db 52 CTCCTCCATCTTCTTC 37

RESULT 9
US-08-474-633A-57/c
; Sequence 57, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE INCREASING THE LYSINE AND THREONINE CONTENT
; TITLE OF INVENTION: OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,633A
; FILING DATE:

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. STEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420

INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: E. coli
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 86-H23
FEATURE:
NAME/KEY: CDS
LOCATION: 2..88
OTHER INFORMATION: /function= "synthetic"

; OTHER INFORMATION: storage protein
; OTHER INFORMATION: /product= "protein"
; OTHER INFORMATION: /gene= "ssp"
; OTHER INFORMATION: /standard_name= "5.8.8.5"
; US-08-474-633A-57

Query Match 0.4%; Score 16; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 CTCCTCCATCTTCTTC 2202
Db 52 CTCCTCCATCTTCTTC 37

RESULT 10
US-08-823-771-57/c
; Sequence 57, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE INCREASING THE LYSINE AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,771
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,633
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. STEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420

INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: E. coli
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 86-H23
FEATURE:
NAME/KEY: CDS
LOCATION: 2..88
OTHER INFORMATION: /function= "synthetic"

/product= "protein"
/gene= "ssp"
/standard_name=
"5.8.8.5"
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-08-823-771-57

Query Match 0.4%; Score 16; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 CTCCTCCATCTTCTTC 2202
|||||
DB 52 CTCCTCCATCTTCTTC 37

RESULT 11

PCT-US92-06412-48/c

; Sequence 48, Application PC/TUS9206412

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; APPLICANT: Janet A. Rice

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing H

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/06412

; FILING DATE: 19920807

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/743,006

; FILING DATE: 9 August 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Linda Axamethy Floyd

; REGISTRATION NUMBER: 33,692

; REFERENCE/DOCKET NUMBER: BB-1031

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 992-4929

; TELEFAX: (302) 892-7949

; TELEX: 835420

; INFORMATION FOR SEQ ID NO: 48:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 97 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; STRAIN: E. coli

; CELL TYPE: DH5 alpha

; IMMEDIATE SOURCE:

; CLONE: 86-H23

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 2...88

; OTHER INFORMATION: /function= "synthetic storage protein

; OTHER INFORMATION: /product= "protein"

; OTHER INFORMATION: /gene= "ssp"

; OTHER INFORMATION: /standard_name= "5.8.8.5"

PCT-US92-06412-48

Query Match 0.4%; Score 16; DB 5; Length 97;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 CTCCTCCATCTTCTTC 2202
|||||
DB 52 CTCCTCCATCTTCTTC 37

RESULT 12

US-08-890-980-64

; Sequence 64, Application US/08890980

; Patent No. 5998141

; GENERAL INFORMATION:

; APPLICANT: Acton, Susan L.

; TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/890,980

; FILING DATE: 10-JUL-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Arnold, Beth E.

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: MIA-005.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 64:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "primer"

US-08-890-980-64

Query Match 0.4%; Score 15; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2777 AGGCTGAAGGAATGA 2791
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DB 4 AGGCTGAAGGAATGA 18

RESULT 13

US-08-890-979-64

; Sequence 64, Application US/08890979

; Patent No. 6030778

; GENERAL INFORMATION:

; APPLICANT: Acton, Susan L.

; APPLICANT: Ordovas, Jose M.

; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,979
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
; US-08-890-979-64

Query Match 0.4%; Score 15; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2777 AGGCTGAAGGAATGA 2791
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Db 4 AGGCTGAAGGAATGA 18

RESULT 14

US-09-032-894-64
; Sequence 64, Application US/09032894
; Patent No. 6130041

; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
; US-09-032-894-64

Query Match 0.4%; Score 15; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 4 AGGCTGAAGGAATGA 18

RESULT 15

US-09-031-626-64
; Sequence 64, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.

; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
; US-09-031-626-64

Query Match 0.4%; Score 15; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2777 AGGCTGAAGGAATGA 2791
|||||
Db 4 AGGCTGAAGGAATGA 18

Search completed: January 11, 2003, 06:08:28
Job time : 121 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 01:49:57 ; Search time 4886 Seconds
(without alignments)
12307.377 Million cell updates/sec

Title: US-10-003-354-3

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Scoring table: OLIGO-MUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database:

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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C 2	23	0.6	91	AZ822704 2M0096K08
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C 6	19	0.5	31	AZ579477 1M0367A08

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C <td>9<td>19<td>0.5<td>89<td>14<td>T52721</td><td>T52721 ya72h02.s1</td></td></td></td></td></td>	9 <td>19<td>0.5<td>89<td>14<td>T52721</td><td>T52721 ya72h02.s1</td></td></td></td></td>	19 <td>0.5<td>89<td>14<td>T52721</td><td>T52721 ya72h02.s1</td></td></td></td>	0.5 <td>89<td>14<td>T52721</td><td>T52721 ya72h02.s1</td></td></td>	89 <td>14<td>T52721</td><td>T52721 ya72h02.s1</td></td>	14 <td>T52721</td> <td>T52721 ya72h02.s1</td>	T52721	T52721 ya72h02.s1
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C <td>15<td>18<td>0.5<td>99<td>14<td>BQ100462</td><td>BQ100462 1109b02.x</td></td></td></td></td></td>	15 <td>18<td>0.5<td>99<td>14<td>BQ100462</td><td>BQ100462 1109b02.x</td></td></td></td></td>	18 <td>0.5<td>99<td>14<td>BQ100462</td><td>BQ100462 1109b02.x</td></td></td></td>	0.5 <td>99<td>14<td>BQ100462</td><td>BQ100462 1109b02.x</td></td></td>	99 <td>14<td>BQ100462</td><td>BQ100462 1109b02.x</td></td>	14 <td>BQ100462</td> <td>BQ100462 1109b02.x</td>	BQ100462	BQ100462 1109b02.x
C <td>16<td>18<td>0.5<td>100<td>12<td>BF173156</td><td>BF173156 MRE0977.M</td></td></td></td></td></td>	16 <td>18<td>0.5<td>100<td>12<td>BF173156</td><td>BF173156 MRE0977.M</td></td></td></td></td>	18 <td>0.5<td>100<td>12<td>BF173156</td><td>BF173156 MRE0977.M</td></td></td></td>	0.5 <td>100<td>12<td>BF173156</td><td>BF173156 MRE0977.M</td></td></td>	100 <td>12<td>BF173156</td><td>BF173156 MRE0977.M</td></td>	12 <td>BF173156</td> <td>BF173156 MRE0977.M</td>	BF173156	BF173156 MRE0977.M
C <td>17<td>17<td>0.5<td>51<td>10<td>AM208717</td><td>AM208717 uc63b06.x</td></td></td></td></td></td>	17 <td>17<td>0.5<td>51<td>10<td>AM208717</td><td>AM208717 uc63b06.x</td></td></td></td></td>	17 <td>0.5<td>51<td>10<td>AM208717</td><td>AM208717 uc63b06.x</td></td></td></td>	0.5 <td>51<td>10<td>AM208717</td><td>AM208717 uc63b06.x</td></td></td>	51 <td>10<td>AM208717</td><td>AM208717 uc63b06.x</td></td>	10 <td>AM208717</td> <td>AM208717 uc63b06.x</td>	AM208717	AM208717 uc63b06.x
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C <td>20<td>17<td>0.5<td>60<td>12<td>BF942724</td><td>BF942724 EST-CD15N</td></td></td></td></td></td>	20 <td>17<td>0.5<td>60<td>12<td>BF942724</td><td>BF942724 EST-CD15N</td></td></td></td></td>	17 <td>0.5<td>60<td>12<td>BF942724</td><td>BF942724 EST-CD15N</td></td></td></td>	0.5 <td>60<td>12<td>BF942724</td><td>BF942724 EST-CD15N</td></td></td>	60 <td>12<td>BF942724</td><td>BF942724 EST-CD15N</td></td>	12 <td>BF942724</td> <td>BF942724 EST-CD15N</td>	BF942724	BF942724 EST-CD15N
C <td>21<td>17<td>0.5<td>60<td>13<td>B1156882</td><td>B1156882 602921624</td></td></td></td></td></td>	21 <td>17<td>0.5<td>60<td>13<td>B1156882</td><td>B1156882 602921624</td></td></td></td></td>	17 <td>0.5<td>60<td>13<td>B1156882</td><td>B1156882 602921624</td></td></td></td>	0.5 <td>60<td>13<td>B1156882</td><td>B1156882 602921624</td></td></td>	60 <td>13<td>B1156882</td><td>B1156882 602921624</td></td>	13 <td>B1156882</td> <td>B1156882 602921624</td>	B1156882	B1156882 602921624
C <td>22<td>17<td>0.5<td>62<td>10<td>AM683571</td><td>AM683571 NF016A06L</td></td></td></td></td></td>	22 <td>17<td>0.5<td>62<td>10<td>AM683571</td><td>AM683571 NF016A06L</td></td></td></td></td>	17 <td>0.5<td>62<td>10<td>AM683571</td><td>AM683571 NF016A06L</td></td></td></td>	0.5 <td>62<td>10<td>AM683571</td><td>AM683571 NF016A06L</td></td></td>	62 <td>10<td>AM683571</td><td>AM683571 NF016A06L</td></td>	10 <td>AM683571</td> <td>AM683571 NF016A06L</td>	AM683571	AM683571 NF016A06L
C <td>23<td>17<td>0.5<td>70<td>13<td>B1452105</td><td>B1452105 G105.A05</td></td></td></td></td></td>	23 <td>17<td>0.5<td>70<td>13<td>B1452105</td><td>B1452105 G105.A05</td></td></td></td></td>	17 <td>0.5<td>70<td>13<td>B1452105</td><td>B1452105 G105.A05</td></td></td></td>	0.5 <td>70<td>13<td>B1452105</td><td>B1452105 G105.A05</td></td></td>	70 <td>13<td>B1452105</td><td>B1452105 G105.A05</td></td>	13 <td>B1452105</td> <td>B1452105 G105.A05</td>	B1452105	B1452105 G105.A05
C <td>24<td>17<td>0.5<td>71<td>9<td>AA422570</td><td>AA422570 v14g10.s</td></td></td></td></td></td>	24 <td>17<td>0.5<td>71<td>9<td>AA422570</td><td>AA422570 v14g10.s</td></td></td></td></td>	17 <td>0.5<td>71<td>9<td>AA422570</td><td>AA422570 v14g10.s</td></td></td></td>	0.5 <td>71<td>9<td>AA422570</td><td>AA422570 v14g10.s</td></td></td>	71 <td>9<td>AA422570</td><td>AA422570 v14g10.s</td></td>	9 <td>AA422570</td> <td>AA422570 v14g10.s</td>	AA422570	AA422570 v14g10.s
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C <td>26<td>17<td>0.5<td>80<td>12<td>BF149230</td><td>BF149230 11.1.Huma</td></td></td></td></td></td>	26 <td>17<td>0.5<td>80<td>12<td>BF149230</td><td>BF149230 11.1.Huma</td></td></td></td></td>	17 <td>0.5<td>80<td>12<td>BF149230</td><td>BF149230 11.1.Huma</td></td></td></td>	0.5 <td>80<td>12<td>BF149230</td><td>BF149230 11.1.Huma</td></td></td>	80 <td>12<td>BF149230</td><td>BF149230 11.1.Huma</td></td>	12 <td>BF149230</td> <td>BF149230 11.1.Huma</td>	BF149230	BF149230 11.1.Huma
C <td>27<td>17<td>0.5<td>80<td>17<td>AZ366225</td><td>AZ366225 1M0115C15</td></td></td></td></td></td>	27 <td>17<td>0.5<td>80<td>17<td>AZ366225</td><td>AZ366225 1M0115C15</td></td></td></td></td>	17 <td>0.5<td>80<td>17<td>AZ366225</td><td>AZ366225 1M0115C15</td></td></td></td>	0.5 <td>80<td>17<td>AZ366225</td><td>AZ366225 1M0115C15</td></td></td>	80 <td>17<td>AZ366225</td><td>AZ366225 1M0115C15</td></td>	17 <td>AZ366225</td> <td>AZ366225 1M0115C15</td>	AZ366225	AZ366225 1M0115C15
C <td>28<td>17<td>0.5<td>81<td>12<td>BG361932</td><td>BG361932 gba9e07.y</td></td></td></td></td></td>	28 <td>17<td>0.5<td>81<td>12<td>BG361932</td><td>BG361932 gba9e07.y</td></td></td></td></td>	17 <td>0.5<td>81<td>12<td>BG361932</td><td>BG361932 gba9e07.y</td></td></td></td>	0.5 <td>81<td>12<td>BG361932</td><td>BG361932 gba9e07.y</td></td></td>	81 <td>12<td>BG361932</td><td>BG361932 gba9e07.y</td></td>	12 <td>BG361932</td> <td>BG361932 gba9e07.y</td>	BG361932	BG361932 gba9e07.y
C <td>29<td>17<td>0.5<td>89<td>14<td>EM731721</td><td>EM731721 sa183c04.y</td></td></td></td></td></td>	29 <td>17<td>0.5<td>89<td>14<td>EM731721</td><td>EM731721 sa183c04.y</td></td></td></td></td>	17 <td>0.5<td>89<td>14<td>EM731721</td><td>EM731721 sa183c04.y</td></td></td></td>	0.5 <td>89<td>14<td>EM731721</td><td>EM731721 sa183c04.y</td></td></td>	89 <td>14<td>EM731721</td><td>EM731721 sa183c04.y</td></td>	14 <td>EM731721</td> <td>EM731721 sa183c04.y</td>	EM731721	EM731721 sa183c04.y
C <td>30<td>17<td>0.5<td>93<td>9<td>AA948071</td><td>AA948071 ok22e10.s</td></td></td></td></td></td>	30 <td>17<td>0.5<td>93<td>9<td>AA948071</td><td>AA948071 ok22e10.s</td></td></td></td></td>	17 <td>0.5<td>93<td>9<td>AA948071</td><td>AA948071 ok22e10.s</td></td></td></td>	0.5 <td>93<td>9<td>AA948071</td><td>AA948071 ok22e10.s</td></td></td>	93 <td>9<td>AA948071</td><td>AA948071 ok22e10.s</td></td>	9 <td>AA948071</td> <td>AA948071 ok22e10.s</td>	AA948071	AA948071 ok22e10.s
C <td>31<td>17<td>0.5<td>93<td>10<td>AM230397</td><td>AM230397 uc63b06.y</td></td></td></td></td></td>	31 <td>17<td>0.5<td>93<td>10<td>AM230397</td><td>AM230397 uc63b06.y</td></td></td></td></td>	17 <td>0.5<td>93<td>10<td>AM230397</td><td>AM230397 uc63b06.y</td></td></td></td>	0.5 <td>93<td>10<td>AM230397</td><td>AM230397 uc63b06.y</td></td></td>	93 <td>10<td>AM230397</td><td>AM230397 uc63b06.y</td></td>	10 <td>AM230397</td> <td>AM230397 uc63b06.y</td>	AM230397	AM230397 uc63b06.y
C <td>32<td>17<td>0.5<td>99<td>9<td>AA257812</td><td>AA257812 MB12S3J3G1</td></td></td></td></td></td>	32 <td>17<td>0.5<td>99<td>9<td>AA257812</td><td>AA257812 MB12S3J3G1</td></td></td></td></td>	17 <td>0.5<td>99<td>9<td>AA257812</td><td>AA257812 MB12S3J3G1</td></td></td></td>	0.5 <td>99<td>9<td>AA257812</td><td>AA257812 MB12S3J3G1</td></td></td>	99 <td>9<td>AA257812</td><td>AA257812 MB12S3J3G1</td></td>	9 <td>AA257812</td> <td>AA257812 MB12S3J3G1</td>	AA257812	AA257812 MB12S3J3G1
C <td>33<td>16<td>0.4<td>19<td>17<td>A2941399</td><td>A2941399 2M0201F07</td></td></td></td></td></td>	33 <td>16<td>0.4<td>19<td>17<td>A2941399</td><td>A2941399 2M0201F07</td></td></td></td></td>	16 <td>0.4<td>19<td>17<td>A2941399</td><td>A2941399 2M0201F07</td></td></td></td>	0.4 <td>19<td>17<td>A2941399</td><td>A2941399 2M0201F07</td></td></td>	19 <td>17<td>A2941399</td><td>A2941399 2M0201F07</td></td>	17 <td>A2941399</td> <td>A2941399 2M0201F07</td>	A2941399	A2941399 2M0201F07
C <td>34<td>16<td>0.4<td>26<td>13<td>BM658913</td><td>BM658913 106602768</td></td></td></td></td></td>	34 <td>16<td>0.4<td>26<td>13<td>BM658913</td><td>BM658913 106602768</td></td></td></td></td>	16 <td>0.4<td>26<td>13<td>BM658913</td><td>BM658913 106602768</td></td></td></td>	0.4 <td>26<td>13<td>BM658913</td><td>BM658913 106602768</td></td></td>	26 <td>13<td>BM658913</td><td>BM658913 106602768</td></td>	13 <td>BM658913</td> <td>BM658913 106602768</td>	BM658913	BM658913 106602768
C <td>35<td>16<td>0.4<td>44<td>17<td>AL760205</td><td>AL760205 Arab1dops</td></td></td></td></td></td>	35 <td>16<td>0.4<td>44<td>17<td>AL760205</td><td>AL760205 Arab1dops</td></td></td></td></td>	16 <td>0.4<td>44<td>17<td>AL760205</td><td>AL760205 Arab1dops</td></td></td></td>	0.4 <td>44<td>17<td>AL760205</td><td>AL760205 Arab1dops</td></td></td>	44 <td>17<td>AL760205</td><td>AL760205 Arab1dops</td></td>	17 <td>AL760205</td> <td>AL760205 Arab1dops</td>	AL760205	AL760205 Arab1dops
C <td>36<td>16<td>0.4<td>48<td>17<td>AZ646970</td><td>AZ646970 1M0513D15</td></td></td></td></td></td>	36 <td>16<td>0.4<td>48<td>17<td>AZ646970</td><td>AZ646970 1M0513D15</td></td></td></td></td>	16 <td>0.4<td>48<td>17<td>AZ646970</td><td>AZ646970 1M0513D15</td></td></td></td>	0.4 <td>48<td>17<td>AZ646970</td><td>AZ646970 1M0513D15</td></td></td>	48 <td>17<td>AZ646970</td><td>AZ646970 1M0513D15</td></td>	17 <td>AZ646970</td> <td>AZ646970 1M0513D15</td>	AZ646970	AZ646970 1M0513D15
C <td>37<td>16<td>0.4<td>50<td>13<td>BJ060889</td><td>BJ060889 BJ060889</td></td></td></td></td></td>	37 <td>16<td>0.4<td>50<td>13<td>BJ060889</td><td>BJ060889 BJ060889</td></td></td></td></td>	16 <td>0.4<td>50<td>13<td>BJ060889</td><td>BJ060889 BJ060889</td></td></td></td>	0.4 <td>50<td>13<td>BJ060889</td><td>BJ060889 BJ060889</td></td></td>	50 <td>13<td>BJ060889</td><td>BJ060889 BJ060889</td></td>	13 <td>BJ060889</td> <td>BJ060889 BJ060889</td>	BJ060889	BJ060889 BJ060889
C <td>38<td>16<td>0.4<td>50<td>17<td>AL759584</td><td>AL759584 Arab1dops</td></td></td></td></td></td>	38 <td>16<td>0.4<td>50<td>17<td>AL759584</td><td>AL759584 Arab1dops</td></td></td></td></td>	16 <td>0.4<td>50<td>17<td>AL759584</td><td>AL759584 Arab1dops</td></td></td></td>	0.4 <td>50<td>17<td>AL759584</td><td>AL759584 Arab1dops</td></td></td>	50 <td>17<td>AL759584</td><td>AL759584 Arab1dops</td></td>	17 <td>AL759584</td> <td>AL759584 Arab1dops</td>	AL759584	AL759584 Arab1dops
C <td>39<td>16<td>0.4<td>54<td>12<td>BG814572</td><td>BG814572 da168h11</td></td></td></td></td></td>	39 <td>16<td>0.4<td>54<td>12<td>BG814572</td><td>BG814572 da168h11</td></td></td></td></td>	16 <td>0.4<td>54<td>12<td>BG814572</td><td>BG814572 da168h11</td></td></td></td>	0.4 <td>54<td>12<td>BG814572</td><td>BG814572 da168h11</td></td></td>	54 <td>12<td>BG814572</td><td>BG814572 da168h11</td></td>	12 <td>BG814572</td> <td>BG814572 da168h11</td>	BG814572	BG814572 da168h11
C <td>40<td>16<td>0.4<td>54<td>14<td>BQ265726</td><td>BQ265726 NISC.f08</td></td></td></td></td></td>	40 <td>16<td>0.4<td>54<td>14<td>BQ265726</td><td>BQ265726 NISC.f08</td></td></td></td></td>	16 <td>0.4<td>54<td>14<td>BQ265726</td><td>BQ265726 NISC.f08</td></td></td></td>	0.4 <td>54<td>14<td>BQ265726</td><td>BQ265726 NISC.f08</td></td></td>	54 <td>14<td>BQ265726</td><td>BQ265726 NISC.f08</td></td>	14 <td>BQ265726</td> <td>BQ265726 NISC.f08</td>	BQ265726	BQ265726 NISC.f08
C <td>41<td>16<td>0.4<td>54<td>17<td>AL758583</td><td>AL758583 Arab1dops</td></td></td></td></td></td>	41 <td>16<td>0.4<td>54<td>17<td>AL758583</td><td>AL758583 Arab1dops</td></td></td></td></td>	16 <td>0.4<td>54<td>17<td>AL758583</td><td>AL758583 Arab1dops</td></td></td></td>	0.4 <td>54<td>17<td>AL758583</td><td>AL758583 Arab1dops</td></td></td>	54 <td>17<td>AL758583</td><td>AL758583 Arab1dops</td></td>	17 <td>AL758583</td> <td>AL758583 Arab1dops</td>	AL758583	AL758583 Arab1dops
C <td>42<td>16<td>0.4<td>57<td>13<td>B1493094</td><td>B1493094 df97f01.y</td></td></td></td></td></td>	42 <td>16<td>0.4<td>57<td>13<td>B1493094</td><td>B1493094 df97f01.y</td></td></td></td></td>	16 <td>0.4<td>57<td>13<td>B1493094</td><td>B1493094 df97f01.y</td></td></td></td>	0.4 <td>57<td>13<td>B1493094</td><td>B1493094 df97f01.y</td></td></td>	57 <td>13<td>B1493094</td><td>B1493094 df97f01.y</td></td>	13 <td>B1493094</td> <td>B1493094 df97f01.y</td>	B1493094	B1493094 df97f01.y
C <td>43<td>16<td>0.4<td>59<td>9<td>A1336716</td><td>A1336716 qw87f05.x</td></td></td></td></td></td>	43 <td>16<td>0.4<td>59<td>9<td>A1336716</td><td>A1336716 qw87f05.x</td></td></td></td></td>	16 <td>0.4<td>59<td>9<td>A1336716</td><td>A1336716 qw87f05.x</td></td></td></td>	0.4 <td>59<td>9<td>A1336716</td><td>A1336716 qw87f05.x</td></td></td>	59 <td>9<td>A1336716</td><td>A1336716 qw87f05.x</td></td>	9 <td>A1336716</td> <td>A1336716 qw87f05.x</td>	A1336716	A1336716 qw87f05.x
C <td>44<td>16<td>0.4<td>60<td>14<td>BQ090810</td><td>BQ090810 ku20e06.y</td></td></td></td></td></td>	44 <td>16<td>0.4<td>60<td>14<td>BQ090810</td><td>BQ090810 ku20e06.y</td></td></td></td></td>	16 <td>0.4<td>60<td>14<td>BQ090810</td><td>BQ090810 ku20e06.y</td></td></td></td>	0.4 <td>60<td>14<td>BQ090810</td><td>BQ090810 ku20e06.y</td></td></td>	60 <td>14<td>BQ090810</td><td>BQ090810 ku20e06.y</td></td>	14 <td>BQ090810</td> <td>BQ090810 ku20e06.y</td>	BQ090810	BQ090810 ku20e06.y
C <td>45<td>16<td>0.4<td>60<td>17<td>CNS03VZ1</td><td>AL263062 Tetradon</td></td></td></td></td></td>	45 <td>16<td>0.4<td>60<td>17<td>CNS03VZ1</td><td>AL263062 Tetradon</td></td></td></td></td>	16 <td>0.4<td>60<td>17<td>CNS03VZ1</td><td>AL263062 Tetradon</td></td></td></td>	0.4 <td>60<td>17<td>CNS03VZ1</td><td>AL263062 Tetradon</td></td></td>	60 <td>17<td>CNS03VZ1</td><td>AL263062 Tetradon</td></td>	17 <td>CNS03VZ1</td> <td>AL263062 Tetradon</td>	CNS03VZ1	AL263062 Tetradon

ALIGNMENTS

RESULT 1
LOCUS AA833564 96 bp mRNA linear EST 31-DEC-1998
DEFINITION aJ45C12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1393270 3',
mRNA sequence.
ACCESSION AA833564
VERSION AA833564.1 GI:2907292
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 96)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNW at:
www-bio.lnlnl.gov/dbtrp/image/image.html
Insert Length: 856 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 55.

FEATURES
source Location/Qualifiers
1. 96
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1393270"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc. and primed with a Not I - oligo(dT) primer [5']
TGTTCACATCTGAGTGGAGCGGCCCAATTTTATTTTATTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonalido."

BASE COUNT 36 a 14 c 8 g 38 t
ORIGIN

Query Match 2.4%; Score 89; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.6e-29;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3625 TTGCTCTACTTGTGATGTTTCAGAAATGCAATATATAAAGTATATATGTTT 3684
|||||
DB 96 TTGCTCTACTTGTGATGTTTCAGAAATGCAATATATAAAGTATATATGTTT 37
|||||

QY 3685 TAATGTAATAACTTAAATGAGTTATTTA 373
|||||

DB 36 TAATGTAATAACTTAAATGAGTTATTTA 8
|||||

RESULT 2
A2822704/c 91 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION 2M0096K08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0096K08 F, DNA sequence.
ACCESSION A2822704
VERSION A2822704.1 GI:12992612
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 91)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weils, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: K column: 08
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 91.
Location/Qualifiers
1. 91
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0096K08"

FEATURES
source Location/Qualifiers
1. 91
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0096K08"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMDA2ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g11473211419b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 28 a 19 c 20 g 24 t
ORIGIN

Query Match 0.6%; Score 23; DB 17; Length 91;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2577 TTTTCTTTCTGAAAAAGCAA 2599
|||||

DB 54 TTTTCTTTCTGAAAAAGCAA 32
|||||

RESULT 3
D18644
LOCUS D18644 74 bp mRNA linear EST 12-DEC-1995
DEFINITION MUSGS01705 Mouse 3'-directed Mus musculus domesticus cDNA clone
md0279 3', mRNA sequence.
ACCESSION D18644
VERSION D18644.1 GI:1100613
KEYWORDS EST.
SOURCE western European house mouse.
ORGANISM Mus musculus domesticus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 74)
Kawamoto, S., Okubo, K., Yoshii, U., Katsuki, M. and Matsubara, K.
Analysis of gene expression in mouse embryogenesis by 3'-directed
cDNA sequencing
Unpublished (1995)
Contact: Kawamoto, S., Okubo, K., Yoshii, U., Katsuki, M. and Matsubara
K.
Institute for Cellular and Molecular Biology
Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.
Location/Qualifiers
1. 74
/organism="Mus musculus domesticus"
/strain="C57BL/6J"
/db_xref="taxon:10092"
/clone="md0279"
/clone_lib="Mouse 3'-directed"
/tissue-type="decidual tissue (day 6.5-8.5 of gestation)"

BASE COUNT 20 a 14 c 17 g 22 t
ORIGIN

Query Match 0.6%; Score 21; DB 14; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3681 GTTTTAATGTAATAACTTTA 3701
|||||

DB 38 GTTTAATGTAATAACTTTA 58

RESULT 4
AM432832/c
LOCUS
DEFINITION AM432832 93 bp mRNA linear EST 03-DEC-2001
shb1f01.y1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1016-6578 5', mRNA sequence.

ACCESSION AM432832
VERSION AM432832.1 GI:6964139
KEYWORDS
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
Glycine.

REFERENCE 1 (bases 1 to 93)
AUTHORS Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp, 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccuteresgen.com
Seq primer: -40RP from GIBCO.
Location/Qualifiers
1..93
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1016-6578"
/clone_1lb="Gm-c1016"
/tissue_type="Immature flowers of field grown plants"
/lab_host="X110-Gold"
/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI. This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into X110-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."

BASE COUNT 29 a 13 c 15 g 36 t
ORIGIN

Query Match 0.5%; Score 20; DB 10; Length 93;
Best Local Similarity 100.0%; Pred. No. 1,1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2564 AGCTTCTCTCTCTTTT 2583
|||||
DB 20 AGCTTCTCTCTCTTTT 1

RESULT 5
A2451477

LOCUS A2451477 99 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0250D23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0250D23 R, DNA sequence.

ACCESSION A2451477
VERSION A2451477.1 GI:10607318
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 99)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Plasmid Inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0250 row: D column: 23
Seq primer: CACACAGCAACACGTCATGACC
Class: plasmid ends
High quality sequence stop: 99.
Location/Qualifiers
1..99
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0250D23"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain X110-Gold, T1-resistant, F-"
/note="Vector: pMD22ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase, and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (g11473211419b1AF139072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 15 c 18 g 54 t
ORIGIN

Query Match 0.5%; Score 20; DB 17; Length 99;
Best Local Similarity 100.0%; Pred. No. 1,1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2566 CTTTCCTCTCTTTT 2585
|||||
DB 23 CTTTCCTCTCTTTT 42

RESULT 6
A2579477/c

LOCUS	AZ579477	31 bp	DNA	linear	GSS 13-DEC-2000
DEFINITION	IM0367A08 Mouse 10kb plasmid library Mus musculus genomic clone tUGC1M0367A08 F, DNA sequence.				
ACCESSION	AZ579477				
VERSION	AZ579477.1	GI:11693906			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 31)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Petersen,T., Rellly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0367 row: A column: 08 Seq primer: CGTGTATAAACGACGCCACAT Class: plasmid ends High quality sequence stop: 31.				

FEATURES
source

```

BASE COUNT
ORIGIN
23 a
      0 c      8 g      0 t
      /organism="Mus musculus"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="U06C1M0367A08"
      /clone_11b="Mouse 10kb plasmid U06C1M library"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaled with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gbl/AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Query Match	0.5%;	Score 19;	DB 17;	Length 31;
Best Local Similarity	100.0%;	Pred. No. 4.1e+03;		
Matches 19; Conservative	0;	Mismatches	0;	Gaps 0;

QY	2568	TTCTTCTTCTTTT	2586
Db	27	TTCTTCTTCTTTT	9

RESULT 7
AZ322055/c

LOCUS	75 bp	DNA	linear	GSS 29-SEP-2000
DEFINITION	1M004211.9 Mouse 10kb plasmid U00C1M library Mus musculus genomic			
ACCESSION	A2322055			
VERSION	A232205			
KEYWORDS	clone U00C1M004211.9 R, DNA sequence.			
SOURCE	A2322055.1 GI:10375410			
ORGANISM	GSS. house mouse. Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, 'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0042 row: L column: 19 Seq primer: CACACAGCAACACGTATGACC Class: plasmid ends High quality sequence stop: 75.			

FEATURES
source

BASE COUNT
ORIGIN

46 a 9 c 15 g 5 t

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0042L15"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g114732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match	0.5%	Score 19	DB 17	length 75
Best Local Similarity	100.0%	Pred. No.	3.4e+03	
Matches 19; Conservative	0	Mismatches	0	Indels 0; Gaps 0

QY	2568	TTCTTCTTCTTTT	2586
Db	69	TTCTTCTTCTTTT	51

RESULT 8
AI810694

LOCUS A1810694 80 bp mRNA linear EST 07-JUL-1999
 DEFINITION tu19h09.x1 NCI CGAP.Pr28 Homo sapiens cDNA clone IMAGE:2251553 3' similar to contains element 11 repetitive element ;, mRNA sequence.
 ACCESSION A1810694
 VERSION A1810694.1 GI:5397260
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 80)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL ac: www-bio.lnl.gov/dbp/image/image.html
 Seq primer: -40bp from G1bco
 High quality sequence stop: 68.
 Location/Qualifiers
 1..80
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2251553"
 /clone_1lb="NCI_CGAP_Pr28"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: prostate; Vector: pUT3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP.Pr28 was prepared, and s circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified from a pool of 5,000 clones made from the same library (clonids 985608-986759, 110192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 3 a 7 c 2 g 68 t
 ORIGIN
 Query Match 0.5%; Score 19; DB 9; Length 80;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2568 TTCTCTCTCTCTTTT 2586
 ||||||||||||||||
 Db 15 TTCTCTCTCTTTT 33
 RESULT 9
 LOCUS T52721/c 99 bp mRNA linear EST 06-FEB-1995
 DEFINITION ya72h02.s1 StrataGene placenta (#937225) Homo sapiens cDNA clone IMAGE:67251 3' similar to similar to gb:x57766_nal STROMELYSIN-3 PRECURSOR (HUMAN), mRNA sequence.
 ACCESSION T52721
 VERSION T52721.1 GI:654581
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 99)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins

M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478
 Other ESTs: ya72h02.r1
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 Insert Size: 1638
 High quality sequence stops: 71 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1638 Std Error: 0.00
 Seq primer: -21m13
 High quality sequence stop: 71.
 Location/Qualifiers
 1..99
 /organism="Homo sapiens"
 /db_xref="GDB:488916"
 /db_xref="taxon:9606"
 /clone="IMAGE:67251"
 /clone_1lb="Stratagene placenta (#937225)"
 /sex="male"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: placenta; Vector: pluescript SK-; Site: 1; EcorI; Site: 2; XhoI; Cloned unidirectionally. Primer: Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GATTTCGCGACAG 3' -3' adaptor sequence: 5' CTCGAGTCTTTT 3."
 BASE COUNT 41 a 14 c 16 g 24 t 4 others
 ORIGIN
 Query Match 0.5%; Score 19; DB 14; Length 99;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2568 TTCTCTCTCTTTT 2586
 ||||||||||||||||
 Db 57 TTCTCTCTCTTTT 39
 RESULT 10
 LOCUS A1207866 31 bp mRNA linear EST 19-OCT-1998
 DEFINITION an06c06.x1 StrataGene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684810 3' similar to SW:YH4_PARIE P15615 HYPOTHETICAL 47.2 KD PROTEIN; contains MER22.t3 MER28 repetitive element ;, mRNA sequence.
 ACCESSION A1207866
 VERSION A1207866
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 31)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Stepoe, M., Tan, F., Theisling, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
 WashU-NCI human EST Project
 Unpublished (1997)
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -400P from Gibco
 High quality sequence stop: 1.

FEATURES

source
 1. .31
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1684810"
 /clone_lib="Stratagene schizo brain S11"
 /sex="male"
 /tissue_type="schizophrenic brain S-11 frontal lobe"
 /dev_stage="34 years old"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Vector: Bluescript SK-; Site_1: EcoRI; Library
 constructed from S-11 frontal lobe, male, 34 years old,
 50% caucasian, 50% Aleutian. Schizophrenic suicide.
 Random primed into EcoRI site of ZAP II Vector. Mass
 excised. Custom library. Avg insert length 1.4kb.
 Material obtained by Johnston N., Torrey, E.F., Yolken R.,
 and the Stanley Neuropathology Consortium - Analysis of
 RNAs from the Brains of Individuals with Psychiatric
 Diseases (unpublished) Stanley Neurovirology Laboratory,
 Johns Hopkins School of Medicine, Baltimore MD."
 1 a 6 c 0 g 24 t

BASE COUNT
 ORIGIN
 Query Match 0.5%; Score 18; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2571 TTCTTCTTTTCTTCT 2588
 Db 7 TTCTTCTTTTCTTCT 24

RESULT 11
 AI422042 37 bp mRNA linear EST 30-MAR-1999
 LOCUS t575705.x1 NCI-CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103344 3'
 DEFINITION Similar to WP:F02E11.2 CE09193; , mRNA sequence.
 ACCESSION AI422042
 VERSION AI422042.1 GI:4267973
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE 1 (bases 1 to 37)
 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BRGAP), Tumor Gene Index
 Unpublished (1998)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsr@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 www-bio.llnl.gov/dbp/image/image.html

Trace considered overall poor quality
 Insert length: 638 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 1.

FEATURES

source
 Location/Qualifiers
 1. .37
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2103344"
 /clone_lib="NCI-CGAP_Brn23"
 /tissue_type="glioblastoma (pooled)"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5',
 TGTTCACATCTGAGGTGGAGCGCCGACATCTTTTCTTTTCTTTTCTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and Eco RI
 the Not I and Eco RI sites of the modified pT73 vector.
 Library is normalized, and was constructed by Bento
 Soares and M. Fatima Bonaldo."
 0 a 7 c 4 g 26 t

BASE COUNT
 ORIGIN
 Query Match 0.5%; Score 18; DB 9; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2571 TTCTTCTTTTCTTCT 2588
 Db 14 TTCTTCTTTTCTTCT 31

RESULT 12
 BF017439/c 67 bp mRNA linear EST 29-DEC-2000
 LOCUS BF017439
 DEFINITION ux73c11.x1 McCarrey Eddy type B spermatogonia Mus musculus cDNA
 clone IMAGE:3654164 3', mRNA sequence.
 ACCESSION BF017439
 VERSION BF017439.1 GI:10748771
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE 1 (bases 1 to 67)
 Maria,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 The Mashu-NCI Mouse EST Project 1999
 Unpublished (1999)
 Other_ESTS: ux73c11.y1
 Contact: Marra M/Mashu-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:416468
 Seq primer: Primer name ambiguous.

FEATURES

source
 Location/Qualifiers
 1. .67
 /organism="Mus musculus"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:3654164"
 /clone_lib="McCarrey Eddy type B spermatogonia"
 /sex="male"
 /tissue_type="type B spermatogonia, pooled from multiple
 mice"
 /dev_stage="8 day"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: testis; Vector: pBluescript SK+ (Stratagene

); Site.1: XhoI; Site.2: EcoRI. cDNA oligo dt'-primed
 [5'-(GA)10-ACTAGTCTCGAGTTTCTTTT-3'] and directionally
 cloned using 5' linkers 5'-AATTCGACGAC-3' and
 5'-CTCGGCGC-3'. Size selection of >400bp material gives
 average insert size ranging from 1-2 kb. Library was mass
 excised (from lambda-UniZAP-XR) and resulting
 single-stranded phagemids were prepped and transformed
 into DH10B. Library contains 96% recombinants.
 References: J. Androl. 20:635-639 and Gene 25:263-269.
 Library constructed and donated by J. McCarrey, Ph.D.
 (Southwest Foundation for Biomedical Research, Dept. of
 Genetics); excision done by E.M. Eddy, Ph.D. (National
 Institutes of Health, National Institute of Environmental
 Health Sciences). Original lambda-based library is
 available through ATCC, catalog #63417."

BASE COUNT 15 a 12 c 15 g 25 t

ORIGIN

Query Match 0.5%; Score 18; DB 12; Length 67;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2961 ACTTACCAATGATTTT 2978
 ||||||||||||||||
 Db 45 ACTTACCAATGATTTT 28

RESULT 13
 BG771352/c 68 bp mRNA linear EST 15-MAY-2001
 LOCUS 602719421F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4840012 5',
 DEFINITION mRNA sequence.
 ACCESSION BG771352
 VERSION BG771352.1 GI:14082005
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 68)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: DCTD/DTP
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LICM1670 row: 1 column: 05
 High quality sequence stop: 60.
 Location/Qualifiers
 1..68
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4840012"
 /clone_lib="NIH_MGC_60"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: prostate; Vector: pNR-LIB (Clontech);
 Site.1: SfiI (ggcgctcgcc); Site.2: SfiI (ggcgctcgcc);
); Double-stranded cDNA was prepared from cell line RNA.
 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGCGCATTAAGCC-3' and 3' adaptor
 sequence: 5'-ATCTAGAGCGCGCGCATTAAG-3' (30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH_MGC

Library."
 BASE COUNT 35 a 15 c 5 g 13 t
 ORIGIN

Query Match 0.5%; Score 18; DB 12; Length 68;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2577 TTTTTCGAAAAA 2594
 ||||||||||||||||
 Db 48 TTTTTCGAAAAA 31

RESULT 14
 B1260363/c 72 bp mRNA linear EST 17-JUL-2001
 LOCUS 602969412F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5108786 5',
 DEFINITION mRNA sequence.
 ACCESSION B1260363
 VERSION B1260363.1 GI:14818593
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 72)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1AM11263 row: h column: 03
 High quality sequence stop: 72.
 Location/Qualifiers
 1..72
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5108786"
 /clone_lib="NIH_MGC_12"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /note="Organ: cervix; Vector: PCMV-SPORT6; Site.1: NotI;
 Site.2: SalI; Cloned unidirectionally. Primer: oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

BASE COUNT 44 a 4 c 6 g 18 t

ORIGIN

Query Match 0.5%; Score 18; DB 13; Length 72;
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2577 TTTTTCGAAAAA 2594
 ||||||||||||||||
 Db 47 TTTTTCGAAAAA 30

RESULT 15
 B0100462/c 99 bp mRNA linear EST 10-APR-2002
 LOCUS B0100462
 DEFINITION 1109b02.x1 Melton Amplified Mouse E16 5 Pancreas 3 M16S1 A Mus
 musculus cDNA clone IMAGE:5941178 3', mRNA sequence.
 ACCESSION B0100462
 VERSION B0100462.1 GI:20133446
 KEYWORDS EST.
 SOURCE house mouse.

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 99)

REFERENCE
 AUTHORS Melton,D., Brown,J., Kenty,G., Permut,A., Lee,C., Kaestner,K.,
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
 ,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvill,I.R., Williams,T.,
 Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other_ESets: 1109b02.y1

TITLE
 JOURNAL
 COMMENT
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biochem.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center This clone is
 available royalty-free through BLNI; please contact the IMAGE
 consortium (info@image.llnl.gov) for further information
 Seq primer: -400P from Gibco
 High quality sequence stop: 84.
 location/Qualifiers
 1. .99

FEATURES
 source
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:5941178"
 /clone_lib="Melton Amplified Mouse E16.5 Pancreas 3 M16S1
 A"
 /sex="Both"
 /tissue_type="pancreas"
 /dev_stage="Embryonic day E16.5"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1;
 Library constructed using Superscript plasmid library kit
 (Life Technologies). cDNA made by oligo-dT priming.
 Size-selected by column fractionation; average insert size
 0.97 kb. Amplified once on solid support. cDNA library
 Preparation: Guolin Chen."

BASE COUNT 21 a 23 c 17 g 38 t

ORIGIN

Query Match 0 5%; Score 18; DB 14; Length 99;
 Best Local Similarity 100.0%; Pred. No. 9e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 2961 ACTTACCAATGAAATTTT 2978
 ||||||||||||||||
 DB 46 ACTTACCAATGAAATTTT 29

Search completed: January 11, 2003, 03:15:09
 Job time : 4892 secs

APPLICANT: Macejak, Dennis
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
FILE REFERENCE: rpi 247/282
CURRENT APPLICATION NUMBER: US/09/504,231A
PRIORITY FILING DATE: 2000-02-15
PRIORITY APPLICATION NUMBER: 09/274,553
PRIORITY FILING DATE: 1999-03-23
PRIORITY APPLICATION NUMBER: 09/257,608
PRIORITY FILING DATE: 1999-02-24
PRIORITY APPLICATION NUMBER: 60/100,842
PRIORITY FILING DATE: 1998-09-18
PRIORITY APPLICATION NUMBER: 60/083,217
PRIORITY FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3242
SOFTWARE: Patentin version 3.0
SEQ ID NO 2705
LENGTH: 36
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-09-504-231A-2705

Query Match 0.4%; Score 16; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 603 CCTCATCAGCCTTGAA 618
DB 16 CCTCATCAGCCTTGAA 1

RESULT 3
US-09-274-553D-2705/c
Sequence 2705, Application US/09274553D
Patent No. US20020082225A1
GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: MCSwigen, James
APPLICANT: Roberts, Beth
APPLICANT: Pavco, Pamela
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
FILE REFERENCE: rpi 247/282
CURRENT APPLICATION NUMBER: US/09/274,553D
PRIORITY FILING DATE: 1999-03-23
PRIORITY APPLICATION NUMBER: 09/257,608
PRIORITY FILING DATE: 1999-02-24
PRIORITY APPLICATION NUMBER: 60/100,842
PRIORITY FILING DATE: 1998-09-18
PRIORITY APPLICATION NUMBER: 60/083,217
PRIORITY FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3148
SOFTWARE: Patentin version 3.0
SEQ ID NO 2705
LENGTH: 36
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-09-274-553D-2705

Query Match 0.4%; Score 16; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 603 CCTCATCAGCCTTGAA 618
DB 16 CCTCATCAGCCTTGAA 1

RESULT 4
US-10-024-997-84
Sequence 84, Application US/10024997
Patent No. US20020150536A1
GENERAL INFORMATION:
APPLICANT: Ruckman, Judy
APPLICANT: Gold, Larry
APPLICANT: Stephens, Andrew
APPLICANT: Janjic, Nebojsa
TITLE OF INVENTION: Nucleic Acid Ligands to Integrins
FILE REFERENCE: NEX82
CURRENT APPLICATION NUMBER: US/10/024,997
PRIORITY FILING DATE: 2001-12-18
PRIORITY APPLICATION NUMBER: 09/364,543
PRIORITY FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 84
LENGTH: 87
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
NAME/KEY: modified_base
LOCATION: (1)-(87)
OTHER INFORMATION: All pyrimidines are 2' F.
US-10-024-997-84

Query Match 0.4%; Score 16; DB 12; Length 87;
Best Local Similarity 75.0%; Pred. No. 6.5e+02;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3350 ATCCACCTGCTTG 3365
DB 23 ATCCACCTGCTTG 38

RESULT 5
US-09-859-214-5
Sequence 5, Application US/09859214
Patent No. US2002010311A1
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MAGCAM-1-MEDIATED
INTERACTIONS AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/859,214
FILING DATE: 16-May-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09/109,879
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/582,740
FILING DATE: 04-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12A2

```
TELECOMMUNICATION INFORMATION:
: TELEPHONE: (781) 861-6240
: TELEFAX: (781) 861-9540
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 36 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-859-214-5

Query Match          0.4%; Score 15; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1449 CCATGATCCATCC 1463
DB 11 CCATGATCCATCC 25

RESULT 6
US-09-205-658-320/c
: Sequence 320, Application US/09205658
: Patent No. US20010029617A1
: GENERAL INFORMATION:
: APPLICANT: Ruvkun, Gary
: TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
: TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
: FILE REFERENCE: 00786/351004
: CURRENT APPLICATION NUMBER: US/09/205,658
: EARLIER FILING DATE: 1998-12-03
: EARLIER APPLICATION NUMBER: 08/857,076
: EARLIER FILING DATE: 1997-05-15
: EARLIER APPLICATION NUMBER: 08/888,534
: EARLIER FILING DATE: 1997-07-07
: EARLIER APPLICATION NUMBER: US98/10080
: EARLIER FILING DATE: 1998-05-15
: NUMBER OF SEQ ID NOS: 328
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 320
: LENGTH: 44
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
US-09-205-658-320

Query Match          0.4%; Score 15; DB 10; Length 44;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 339 CGAGAGAGAGAGA 353
DB 36 CGAGAGAGAGAGA 22

RESULT 7
US-09-756-095-71
: Sequence 71, Application US/09756095
: Patent No. US20020115207A1
: GENERAL INFORMATION:
: APPLICANT: Mitchell, Lloyd G.
: APPLICANT: Garcia-Blanco, Mariano A.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
: TITLE OF INVENTION: SPLICOSOME MEDIATED RNA TRANS-SPLICING
: FILE REFERENCE: A31304-B-A 072874.0134
: CURRENT APPLICATION NUMBER: US/09/756,095
: PRIOR FILING DATE: 2001-01-08
: PRIOR APPLICATION NUMBER: 09/158,863
: PRIOR FILING DATE: 1998-09-23
: PRIOR APPLICATION NUMBER: 09/133,717
: PRIOR FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: 09/087,233
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: PRIOR FILING DATE: 1998-05-28
: PRIOR APPLICATION NUMBER: 08/766,354
: PRIOR FILING DATE: 1996-12-13
: PRIOR APPLICATION NUMBER: 60/008,317
: PRIOR FILING DATE: 1995-12-07
: NUMBER OF SEQ ID NOS: 105
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 71
: LENGTH: 47
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Branch point, pyrimidine tract and acceptor splice
: OTHER INFORMATION: site of PTM
US-09-756-095-71

Query Match          0.4%; Score 15; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2572 TCTCTTTTCTTTT 2586
DB 15 TCTCTTTTCTTTT 29

RESULT 8
US-09-946-807-1323
: Sequence 1323, Application US/09946807
: Patent No. US20020165144A1
: GENERAL INFORMATION:
: APPLICANT: Stefansson, Hreinn
: APPLICANT: Steinthorsdottir, Valgerdur
: APPLICANT: Gulcher, Jeffrey R.
: TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
: FILE REFERENCE: 2345.2004-001
: CURRENT APPLICATION NUMBER: US/09/946,807
: CURRENT FILING DATE: 2001-09-05
: PRIOR APPLICATION NUMBER: US/09/795,668
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: US 09/515,716
: PRIOR FILING DATE: 2000-02-28
: NUMBER OF SEQ ID NOS: 1531
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1323
: LENGTH: 61
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-946-807-1323

Query Match          0.4%; Score 15; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3628 CCTCTACTTTGTATT 3642
DB 12 CCTCTACTTTGTATT 26

RESULT 9
US-09-795-668-1323
: Sequence 1323, Application US/09795668
: Patent No. US20020045577A1
: GENERAL INFORMATION:
: APPLICANT: Stefansson, Hreinn
: APPLICANT: Steinthorsdottir, Valgerdur
: APPLICANT: Gulcher, Jeffrey R.
: TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
: FILE REFERENCE: 2345.2004-001
: CURRENT APPLICATION NUMBER: US/09/795,668
: CURRENT FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: US 09/515,716
: PRIOR FILING DATE: 2000-02-28
: NUMBER OF SEQ ID NOS: 1531
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SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1323
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-1323

Query Match 0.4%; Score 15; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3628 CCTCTACTTGTATT 3642
DB 12 CCTCTACTTGTATT 26

RESULT 10
US-09-795-686-1323
; Sequence 1323, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinhorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345,2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1323
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-686-1323

Query Match 0.4%; Score 15; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3628 CCTCTACTTGTATT 3642
DB 12 CCTCTACTTGTATT 26

RESULT 11
US-10-076-248-13
; Sequence 13, Application US/10076248
; Publication No. US20020135580A1
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Lloyd
; APPLICANT: Garcia-Blanco, Mariano
; APPLICANT: Puttaraju, Madalain
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
; FILE REFERENCE: A31304B-A-F 069906,0105
; CURRENT APPLICATION NUMBER: US/10/076,248
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 09/941,492
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 09/838,858
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/756,096
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/158,863
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 09/133,717
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 09/087,233
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 08/766,354

; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: 60/008,317
; PRIOR FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P1M branch point, polypyrimidine tract and
; OTHER INFORMATION: acceptor splice site
US-10-076-248-13

Query Match 0.4%; Score 15; DB 9; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2572 TCTTCTTTTCTTTT 2586
DB 15 TCTTCTTTTCTTTT 29

RESULT 12
US-09-920-300A-1268/C
; Sequence 1268, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121,547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1268
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 53
; OTHER INFORMATION: n = A,T,C or G
US-09-920-300A-1268

Query Match 0.4%; Score 15; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2602 AGCACACGACACACA 2616
DB 68 AGCACACGACACACA 54

RESULT 13
US-10-033-528-1268/C
; Sequence 1268, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121,547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896

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SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1268
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 53
; OTHER INFORMATION: n = A,T,C or G
US-10-033-528-1268

Query Match          0.4%; Score 15; DB 12; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2602 AGCACACAGCACACA 2616
Db 68 AGCACACAGCACACA 54

RESULT 14
US-09-864-761-31308/C
; Sequence 31308, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31308
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; LENGTH: 75
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC018516.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.49
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.48
US-09-864-761-31308

Query Match          0.4%; Score 15; DB 10; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2568 TTCTCTCTCTTTT 2582
Db 17 TTCTCTCTCTTTT 3

RESULT 15
US-09-878-574-6583
; Sequence 6583, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 6583
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701098625H1
US-09-878-574-6583

Query Match          0.4%; Score 15; DB 10; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2198 TTTCTCTGAAGAAGA 2212
Db 53 TTTCTCTGAAGAAGA 67

Search completed: January 11, 2003, 06:06:14
Job time : 154 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 01:51:27 ; Search time 717 Seconds
(without alignments)
11652.022 Million cell updates/sec

Title: US-10-003-354-3

Perfect score: 3713
Sequence: 1 attaacagcgccgctggttaag.....aaacttaatgagtattatta 3713

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database: N_Geneseq_101002.*

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3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	1.6	60	ABNA1013	Human spliced tran
2	19	0.5	50	ABLO1023	Human SNP Involvin
3	18	0.5	36	AAQ25486	Purine rich HUMINT
4	18	0.5	51	AAH40868	Human SNP flanking
5	18	0.5	60	ABNA1363	Human spliced tran
6	17	0.5	25	AAAC96031	HLA HLA-C gene PCR
7	17	0.5	33	AAH46165	Hexokinase protein
8	17	0.5	38	AAH40778	Primer for Hpv6a L
9	17	0.5	41	AAH46167	Hexokinase protein

10	17	0.5	41	22	AAH46168	Hexokinase protein
c 11	17	0.5	48	18	AAH88795	Feline parvoviral
c 12	17	0.5	51	22	AAH39316	Human SNP flanking
13	17	0.5	54	17	AAH64429	Human stromelysin
14	17	0.5	82	16	AAH29416	Human gene signatu
15	16	0.4	24	16	AAH41135	Human gene signatu
16	16	0.4	24	20	AAH79281	Sequence VI to con
17	16	0.4	24	20	AAH79283	Generic HCV NS3 pr
c 18	16	0.4	25	21	AAAC96111	16S rRNA gene PCR
19	16	0.4	25	21	AAAC96228	16S rRNA gene PCR
20	16	0.4	26	22	AAH14655	Human voltage-gate
c 21	16	0.4	28	19	AAH09936	Human biallelic po
22	16	0.4	47	21	AAH67873	Human map-related
c 23	16	0.4	51	22	AAH32726	Human SNP oligonuc
c 24	16	0.4	51	22	AAH73745	Human silent SNP c
c 25	16	0.4	52	18	AAH76376	Staphylococcus aur
26	16	0.4	53	21	AAH18812	Human secreted pro
27	16	0.4	59	21	AAH23038	Human secreted pro
c 28	16	0.4	60	24	ABN36070	Human spliced tran
c 29	16	0.4	60	24	ABN37919	Human spliced tran
c 30	16	0.4	60	24	ABNA7890	Human spliced tran
c 31	16	0.4	64	19	AAH73253	C. utilis crti pri
c 32	16	0.4	65	24	ABN30103	Rat spliced transcr
c 33	16	0.4	66	19	AAH73251	C. utilis crti pri
c 34	16	0.4	73	20	AAH79285	HCV NS3 protease 1
c 35	16	0.4	74	20	AAH79282	Generic HCV NS3 pr
36	16	0.4	74	20	AAH79286	HCV NS3 protease 1
37	16	0.4	74	20	AAH79287	HCV NS3 protease 1
38	16	0.4	87	22	AAH73723	HGF nucleic acid 1
39	16	0.4	87	24	ABK31633	Integrin alpha v b
c 40	16	0.4	95	21	AAH14899	Antisense strand n
c 41	16	0.4	97	14	AAH37275	Clone 86-H23 used
c 42	16	0.4	97	16	AAH94994	SSP 5.8-8.5 clone
c 43	16	0.4	97	19	AAH35832	Synthetic storage
c 44	16	0.4	97	20	AAH95529	Synthetic lysine-r
c 45	15	0.4	17	21	AAH03348	Hammerhead ribozym

ALIGNMENTS

```
RESULT 1
ABNA1013
ID ABNA1013 standard; DNA; 60 BP.
AC ABNA1013:
XX
XX 15-JUL-2002 (first entry)
DT
DT Human spliced transcript detection oligonucleotide SEQ ID NO:13761.
DE
DE Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
KW
KW Homo sapiens.
OS
OS
OS WO200210449-A2.
PM
PM 07-FEB-2002.
PD
PD 20-JUL-2001; 2001WO-1B01903.
PF
PF 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
PA
PA Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI WPI. 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
PT
```

PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 13761; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN53589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 23 A; 15 C; 15 G; 7 T; 0 other;
XX
Query Match 1.6%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.4e-19;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1130 AATATGACCTCAAGGCTCACTACAAAGCGGCGCTCCGAGAAAGCGAGAGAG 1189
DB 1 AATATGACCTCAAGGCTCACTACAAAGCGGCGCTCCGAGAAAGCGAGAGAG 60
XX
RESULT 2
ABLO1023
ID ABL01023 standard; DNA; 50 BP.
XX
AC ABL01023;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human SNP involving a gap oligonucleotide SEQ ID NO:1014.
XX
KM Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KM immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KM autoimmune disease; inflammation; cancer; nervous system disease;
KM infection; polymorphic protein; ds.
XX
OS Homo sapiens.
XX
OS WO200138586-A2.
XX
PN 31-MAY-2001.
XX
PD 22-NOV-2000; 2000WO-US32311.
XX
PF 22-NOV-1999; 99US-0167383.
XX
PR 24-NOV-1999;
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-355949/37.
XX
PT Isolated human nucleic acids comprising one or more single nucleotide

PT polymorphisms, useful for treating a subject suffering from a
PT pathology, e.g. autoimmune diseases, ascribed to the presence of a
PT sequence polymorphism -
XX
PS Claim 1; Page 554; 674pp; English.
XX
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the
CC polymorphic protein within appropriate physiological samples).
XX
SQ Sequence 50 BP; 1 A; 11 C; 2 G; 36 T; 0 other;
XX
Query Match 0.5%; Score 19; DB 23; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2567 TTCTCTCTCTCTTTT 2585
DB 8 TTCTCTCTCTCTTTT 26
XX
RESULT 3
AAQ25486/C
ID AAQ25486 standard; DNA; 36 BP.
XX
AC AAQ25486;
XX
DT 07-DEC-1992 (first entry)
XX
DE Purine rich HOMINT02 target duplex sequence.
XX
KM Target; human leukocyte adhesion protein p150,95 alpha subunit
KM gene; AIDS; triplex; HIV; hepatitis; malignancy; inflammation; ds.
XX
OS Synthetic.
XX
PN WO9209705-A.
XX
PD 11-JUN-1992.
XX
PF 25-NOV-1991; 91MO-US08811.
XX
XX 23-NOV-1990; 90US-0617907.
XX 18-JAN-1991; 91US-0643382.
XX 08-APR-1991; 91US-0683420.
XX 17-APR-1991; 91US-0686544.
XX 17-APR-1991; 91US-0686546.
XX 17-APR-1991; 91US-0686547.
XX 27-SEP-1991; 91US-0766733.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Froehner B, Krawczyk S, Matteucci MD, Milligan J;
XX
DR WPI; 1992-217083/26.
XX
PT New oligomers contg. modified bases - which form a triplex with
PT G-C doublet in a DNA duplex, for treating and diagnosing HIV,
PT hepatitis, herpes, malignancy and inflammation
XX

PS Claim 11; Page 64; 77pp; English.

XX The sequence depicts a HUMINT02 sequence beginning at nucleotide
CC 2370. The sequence is a viral duplex sequence which contains a
CC purine-rich region concentrated on one chain of the duplex. The
CC sequence may be prepred. by standard DNA synthesis. The HUMINT02
CC duplex sequence is used as a target for novel oligomers which are
CC capable of forming a triplex at physiological pH by coupling into
CC the major groove of the DNA duplex. Two such oligomers LAP
CC 321-2 are capable of forming a triplex with this sequence. The
CC oligomers are used in the treatment of inflammation. Similar oligomers
CC may be used to target viral DNA duplexes specific for HIV, herpes and
CC other viruses. The triple helices form under mild conditions thus
CC assays may be carried out without subjecting the test specimen to
CC harsh conditions. The oligomer is able to inhibit gene expression,
CC as verified by in vitro systems.
CC See also AA025452-25501 and AA030226-448.

XX
XX Sequence 36 BP; 27 A; 0 C; 9 G; 0 U; 0 other;

SQ

Query Match 0.5%; Score 18; DB 13; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2568 TTCTCTCTCTTTT 2585
|||||
DB 18 TTCTCTCTCTTTT 1

RESULT 4
AAH40868
ID AAH40868 standard; DNA; 51 BP.
XX
AC AAH40868;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 3664.
XX
KW Single nucleotide; agammaglobulinemia; diabetes insipidus; cancer;
KW SNGP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KW Leesh-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; ds.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US28436.
XX
PR 15-OCT-1999; 99US-0160096.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI: 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample
XX
PS Claim 1; Page 68; 83pp; English.

CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a

CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Leesh-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
CC DNA flanking the site of a single nucleotide polymorphism.

XX
XX Sequence 51 BP; 5 A; 15 C; 8 G; 23 T; 0 other;

SQ

Query Match 0.5%; Score 18; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2567 TTCTCTCTTTT 2584
|||||
DB 34 TTCTCTCTTTT 51

RESULT 5
ABN41363
ID ABN41363 standard; DNA; 60 BP.
XX
AC ABN41363;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:14111.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI: 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
PS Example 1; SEQ ID 14111; 47pp; English.

CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of

CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialized mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 11 A; 21 C; 15 G; 13 T; 0 other;

Query Match 0.5%; Score 18; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2727 TGCCAGAGACGCTCTC 2744
18 TGCCAGAGACGCTCTC 35
Db

RESULT 6
AAC96031
ID AAC96031 standard; DNA; 25 BP.
AC AAC96031;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-C gene PCR primer #43.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP03636.
XX
PR 26-APR-1999; 99EP-0303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences
PT of specific length -
XX
PS Claim 14; Page 44; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in

CC particular.
XX
SQ Sequence 25 BP; 1 A; 5 C; 2 G; 17 T; 0 other;

Query Match 0.5%; Score 17; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2999 TTTTTCGCTCTC 3015
6 TTTTTCGCTCTCTC 22
Db

RESULT 7
AAH46165
ID AAH46165 standard; DNA; 33 BP.
XX
AC AAH46165;
XX
DT 21-SEP-2001 (first entry)
XX
DE Hexokinase protein 12 PCR primer, SEQ ID NO:5.
XX
XX Hexokinase protein 12; human; recombinant production;
KW malignant tumour; cancer; blood disease; HIV infection;
KW human immunodeficiency virus; immune disorder; inflammatory condition;
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200147968-A1.
XX
PD 05-JUL-2001.
XX
PF 18-DEC-2000; 2000WO-CN00597.
XX
PR 23-DEC-1999; 99CN-0125723.
XX
PA (UYFU-) UNIV FUDAN.
PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-418227/44.
XX
PT Hexokinase protein 12 and encoded polynucleotide, applicable in
PT diagnosis and treatment of cancer, hemopathy, HIV infection,
PT immunological diseases and phlogosis -
XX
PS Example 5; Page 17; 35pp; Chinese.
XX
CC The invention relates to hexokinase protein 12 (AAH3785), nucleic acids
CC encoding it (AAH46162), and a method for the recombinant production of
CC hexokinase protein 12. The present invention additionally discloses an
CC antagonist of hexokinase protein 12 for therapeutic use, and an antibody
CC which specifically binds to hexokinase protein 12. Hexokinase protein 12,
CC and nucleotides which encode it may be used for treating a variety of
CC diseases, such as malignant tumours, blood diseases, HIV (human
CC immunodeficiency virus) infection, immune disorders and inflammatory
CC conditions. The protein may also be used to screen for modulators of its
CC activity or for peptide fingerprinting identification. The polynucleotide
CC can be used as a primer for nucleic acid amplification reactions or as a
CC probe for hybridisation reactions, or in producing gene chips or
CC microarrays. Sequences AAH46165-AAH46166 represent PCR primers used in
CC an exemplification of the invention to amplify human hexokinase protein
CC 12 cDNA for cloning.
XX
SQ Sequence 33 BP; 9 A; 6 C; 9 G; 9 T; 0 other;

Query Match 0.5%; Score 17; DB 22; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2692 CATGGTGTATGAGA 2708
|||
DB 16 CATGGTGTATGAGA 32

RESULT 8

AAT40778/c
ID AAT40778 standard; CDNA; 38 BP.

AC AAT40778;

XX 26-NOV-1996 (first entry)

DE primer for HPV6a L2 gene amplification.

XX MN9; yeast; disrupt; human papilloma virus; capsid protein;
KM prevent; vaccine; infection; treat; primer; PCR; probe; ss.

OS Synthetic.

PN MO9615247-A1.

XX 23-MAY-1996.

XX 13-NOV-1995; 95WO-US15027.

XX 14-NOV-1994; 94US-0339368.

XX (MERI) MERCK & CO INC.

PI Cook JC, George HA, Hofmann KJ, Jansen KU, Joyce JG;
PI Lehman ED, Markushz, Schultz LD;

XX WPI; 1996-268219/27.

XX Papilloma: virus capsid proteins, pref. L1, L2, L1 + L2 and derivs. -
PT useful in vaccines to treat or prevent papillomavirus infection

XX Example 14; Page 30; 92pp; English.

CC AAT40774-78 are primers used in the cloning of human papilloma virus
CC (HPV) strain 6a capsid protein genes L1, L2 and L1+L2. Yeast strains
CC contg. disrupted genes (see AAT40768-73) were used for the isolation of
CC HPV capsid proteins. The capsid proteins are useful in vaccines to treat
CC or prevent HPV infection. The present sequence is a 3' antisense primer
CC used to amplify the HPV6a L2 gene.

XX Sequence 38 BP; 12 A; 12 C; 9 G; 5 T; 0 other;

Query Match 0.5%; Score 17; DB 17; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 70 TTTTTCAGATGCGC 86
|||
DB 33 TTTTTCAGATGCGC 17

RESULT 9

AAH46167
ID AAH46167 standard; DNA; 41 BP.

AC AAH46167;

XX 21-SEP-2001 (first entry)

DE Hexokinase protein 12 probe, SEQ ID NO:8.

XX Hexokinase protein 12; human; recombinant production;
KM malignant tumour; cancer; blood disease; HIV infection;

KW human immunodeficiency virus; immune disorder; inflammatory condition;
KM cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.

OS Homo sapiens.

PN WO200147968-A1.

XX 05-JUL-2001.

XX 18-DEC-2000; 2000WO-CN00597.

XX 23-DEC-1999; 99CN-0125723.

PA (YUFU-) UNIV FUDAN.

PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.

PI Mao Y, Xie Y;

XX WPI; 2001-418227/44.

XX Hexokinase protein 12 and encoded polynucleotide, applicable in
PT diagnosis and treatment of cancer, hemopathy, HIV infection,
PT immunological diseases and phlogosis

XX Example 7; Page 20; 35pp; Chinese.

CC The invention relates to hexokinase protein 12 (AAB73785), nucleic acids
CC encoding it (AAH46162), and a method for the recombinant production of
CC hexokinase protein 12. The present invention additionally discloses an
CC antagonist of hexokinase protein 12 for therapeutic use, and an antibody
CC which specifically binds to hexokinase protein 12. Hexokinase protein 12,
CC and nucleotides which encode it may be used for treating a variety of
CC diseases, such as malignant tumours, blood diseases, HIV (human
CC immunodeficiency virus) infection, immune disorders and inflammatory
CC conditions. The protein may also be used to screen for modulators of its
CC activity or for peptide fingerprinting identification. The polynucleotide
CC can be used as a primer for nucleic acid amplification reactions or as a
CC probe for hybridisation reactions, or in producing gene chips or
CC microarrays. Sequences AAH46167-AAH46168 represent hexokinase protein 12
CC probes used in an exemplification of the invention.

XX Sequence 41 BP; 7 A; 7 C; 12 G; 15 T; 0 other;

Query Match 0.5%; Score 17; DB 22; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2692 CATGGTGTATGAGA 2708
|||
DB 6 CATGGTGTATGAGA 22

RESULT 10

AAH46168
ID AAH46168 standard; DNA; 41 BP.

AC AAH46168;

XX 21-SEP-2001 (first entry)

DE Hexokinase protein 12 probe, SEQ ID NO:9.

XX Hexokinase protein 12; human; recombinant production;
KM malignant tumour; cancer; blood disease; HIV infection;

KW human immunodeficiency virus; immune disorder; inflammatory condition;
KM cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.

OS Homo sapiens.

PN WO200147968-A1.

XX 05-JUL-2001.

XX 18-DEC-2000; 2000WO-CN00597.

XX 23-DEC-1999; 99CN-0125723.

DR WP1: 1997-535847/49.
DR P-PSDB: AAM311733.
XX
PT Vaccine containing nucleic acid expressing parvoviral epitope -
PT particularly both B and T cell epitope(s), for immunisation of cats,
PT dogs and mink against parvoviruses, also as a carrier for other
PT antigens
XX
PS Claim 12; Page 15; 30pp; English.
XX
CE This synthetic nucleotide sequence encodes the T-cell epitope of a
CE parvoviral VP1 nucleocapsid protein. This is used in the preparation of
CE an anti-parvovirus vaccine. The anti-parvovirus vaccine contains nucleic
CE acid encoding at least one parvovirus-specific VP1 or VP2 T/B cell
CE antigenic epitope plus a carrier. The anti parvovirus vaccine are
CE especially used to protect cats, dogs and mink, e.g. against feline
CE panleukopenia virus, mink enteritis virus or gastroenteritis caused by
CE canine parvovirus (CPV). The vaccine also includes an adjuvant,
CE particularly a DNA containing unethylated CPG motifs i.e. ISO. The ISO
CE contains phosphorothioate linkages and is a powerful immune activator.
CE The vaccine may also be used to deliver other immunogens, e.g. (human)
CE hepatitis B surface antigen. Immunisation with naked DNA provides good
CE protection against parvovirus after only one injection. Both humoral and
CE cellular responses may be induced.
S0 Sequence 48 BP; 19 A; 11 C; 9 G; 9 T; 0 other;
XX
Query Match 0.5%; Score 17; DB 18; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY 2562 CCAGCTTCTCTCTCTT 2578
XXXXXXXXXXXXXXXXXXXX
DB 47 CCAGCTTCTCTCTCTT 31
XXXXXXXXXXXXXXXXXXXX
RESULT 12
ID AAH39316/c
ID AAH39316 standard; DNA; 51 BP.
AC AAH39316;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 2112.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KW Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; ds.
OS Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US28436.
XX
XX 15-OCT-1999; 99US-0160096.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Piconult-Newburg L, Pohl M;
XX
XX WP1: 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample
XX

PS Claim 1; Page 60; 83bp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
CC DNA flanking the site of a single nucleotide polymorphism.
XX
SQ Sequence 51 BP; 20 A; 9 C; 7 G; 15 T; 0 other;
XX
Query Match 0.5%; Score 17; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2577 TTTTTCGAAAA 2593
XXXXXXXXXXXXXXXXXXXX
DB 19 TTTTTCGAAAA 3
XXXXXXXXXXXXXXXXXXXX
RESULT 13
AAH64429
ID AAH64429 standard; RNA; 54 BP.
XX
AC AAH64429;
XX
DT 20-JUL-1999 (first entry)
XX
DE Human stromelysin hairpin ribozyme SEQ ID NO:1061.
XX
KW Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN MO9618736-A2.
XX
PD 20-JUN-1996.
XX
PF 22-NOV-1995; 95WO-0515516.
XX
XX 05-OCT-1995; 95US-0541365.
PR 13-DEC-1994; 94US-0354920.
PR 23-DEC-1994; 94US-0363253.
PR 23-DEC-1994; 94US-0363256.
PR 17-FEB-1995; 95US-0390850.
PR 20-APR-1995; 95US-0426124.
PR 02-MAY-1995; 95US-0432874.
PR 04-MAY-1995; 95US-0434509.
PR 07-JUL-1995; 95US-0000951.
PR 07-JUL-1995; 95US-0000974.
PR 07-AUG-1995; 95US-0512861.
XX

XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DT;
PI Bejelman L, Karpelsky A, Modak A, Usman N, Burgin A;
PI Matlic-Adamic J, Jarvis T, Thompson JD, Wincott F;
XX
DR WPI; 1996-300653/30.
XX
PT Enzymatic nucleic acid molecules having a hammer-head motif - used
PT for the treatment of arthritis, induction of graft tolerance or
PT treatment of auto-immune diseases
XX
PS Example 1; Page 164; 307bp; English.
XX
XX The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose
CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)
CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.
CC The ENA's can inhibit collagenase and stromelysin production in the
CC synovial membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 54 BP; 18 A; 9 C; 18 G; 9 U; 0 other;
XX
Query Match 0.5%; Score 17; DB 17; Length 54;
Best Local Similarity 94.1%; Pred. No. 1.1e+03;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3286 TCAGGGGAGAGAGGGCG 3302
:XXXXXXXXXXXXXXXXXX
DB 1 DCAGGGGAGAGAGGGCG 17
XXXXXXXXXXXXXXXXXXXX
RESULT 14
AAT20416
ID AAT20416 standard; CDNA to mRNA; 82 BP.
XX
AC AAT20416;
XX
DT 19-JUL-1996 (first entry)
XX
DE Human gene signature HDNGS01570.
XX
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; Cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
XX
OS Homo sapiens.
OS Homo sapiens.
XX
PN WO9514772-A1.
XX
PD 01-JUN-1995.
XX
PF 11-NOV-1994; 94WO-JP01916.
PR 12-NOV-1993; 93JP-0355504.
XX
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
XX
PI Matsubara K, Okubo K;
XX

```

XX
DR WPI, 1995-206931/27.
XX
XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
XX
PS Claim 1; Page 632; 2245pp; Japanese.
XX
XX A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in AAT19001-T26837 and which is able to hybridize to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridize with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
XX
SQ Sequence 82 BP; 31 A; 7 C; 14 G; 30 T; 0 other;
Query Match 0.5%; Score 17; DB 16; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2521 TCTGTAAGGTTTGG 2537
DB 7 TCTGTAAGGTTTGG 23
RESULT 15
AAT41135
ID AAT41135 standard; DNA; 24 BP.
XX
AC AAT41135;
XX
DT 03-DEC-1996 (first entry)
XX
DE Human gene signature HUMGS01570-derived sense primer.
XX
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; primer; PCR; amplification;
KW polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN WO9514772-A1.
XX
PD 01-JUN-1995.
XX
PE 11-NOV-1994; 94WO-JP01916.
XX
PR 12-NOV-1993; 93JP-0355504.
XX
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
XX
PI Matsubara K, Okubo K;
XX
DR WPI, 1995-206931/27.
XX
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues

```

```

XX
PS Example 7; Fig 7; 2245pp; Japanese.
XX
CC Primers T41001-T41382 are derived from novel human gene signature (GS)
CC sequences which did not match with sequences deposited in Genbank release
CC 76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA
CC libraries prepared from various human tissues; synthesis of cDNA was
CC initiated from the 3'-end of mRNA by using poly(T) as the sole primer.
CC Each library is constructed so as to reflect accurately the relative
CC abundance of different mRNAs in the particular tissue from which it was
CC derived. The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS sequences)
CC as a means of diagnosing abnormal cell function or for recognising
CC different cell types. The primers T41135-6 amplify clone pm2810 which
CC comprises the GS HUMGS001570 (T20570), located on chromosome 11.
XX
SQ Sequence 24 BP; 6 A; 1 C; 6 G; 11 T; 0 other;
Query Match 0.4%; Score 16; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2522 CTGTAAGGTTTGG 2537
DB 1 CTGTAAGGTTTGG 16
Search completed: January 11, 2003, 03:27:17
Job time : 719 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 01:52:33 ; Search time 9356 Seconds
(without alignments)
11549.671 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

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Word size: 0

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_plo:*
35: em_hlg_rtd:*
36: em_hlg_mam:*
37: em_hlg_vrl:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID
← length of
region of 100% match

Result No.	Score	Query Match	Length	DB ID	Description
1	20	0.5	83	9	HUMSPALTC
2	19	0.5	50	6	AX165819
3	18	0.5	51	6	AX118541
4	17	0.5	25	6	AX042894
5	17	0.5	42	6	AX3509
6	17	0.5	48	6	AX3513
7	17	0.5	48	6	AX3514
8	17	0.5	51	6	AX116989
9	17	0.5	54	6	AX18031
10	17	0.5	54	6	AX1881
11	17	0.5	65	6	AX482998
12	16	0.4	24	6	E25574
13	16	0.4	25	6	E25576
14	16	0.4	25	6	AX042974
15	16	0.4	25	6	AX043091
16	16	0.4	28	6	AX73896
17	16	0.4	32	6	AX037332
18	16	0.4	51	6	AX157358
19	16	0.4	64	10	RATANSAND
20	16	0.4	65	6	AX486185
21	16	0.4	65	6	AX486614
22	16	0.4	74	6	E25575
23	16	0.4	97	6	AR014618
24	16	0.4	97	6	BD010410
25	16	0.4	97	6	I26751
26	16	0.4	98	9	HUMNTGCF4
27	15	0.4	17	6	AX216771
28	15	0.4	18	6	AX7837
29	15	0.4	18	6	AR092040
30	15	0.4	18	6	AR112175
31	15	0.4	18	6	AR149217
32	15	0.4	18	6	AX428715
33	15	0.4	19	6	AR082444
34	15	0.4	19	6	AR139000
35	15	0.4	19	6	AX039816
36	15	0.4	20	6	AX296645
37	15	0.4	22	6	I46655
38	15	0.4	24	6	AX292012
39	15	0.4	24	6	AX377075
40	15	0.4	24	6	AX444522
41	15	0.4	25	6	AX135862
42	15	0.4	26	6	AX038118
43	15	0.4	26	6	AX038119
44	15	0.4	27	6	AX286269
45	15	0.4	27	6	E09727

ALIGNMENTS

RESULT 1
HUMSPALTC/c 83 bp mRNA linear PRI 13-FEB-2002
LOCUS
DEFINITION Homo sapiens nuclear autoantigen mRNA, partial cds; alternatively spliced.
ACCESSION L79986.1 GI:18653899
VERSION Spi100; alternative splicing; interferon-inducible protein; nuclear autoantigen.
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 83)
Szosteckl,C., Guldner,H.H., Netter,H.J. and Will,H.

TITLE Isolation and characterization of cDNA encoding a human nuclear antigen predominantly recognized by autoantibodies from patients with primary biliary cirrhosis
JOURNAL J. Immunol. 145 (12), 4338-4347 (1990)
MEDLINE 91079525
PUBMED 2258622
REFERENCE 2 (bases 1 to 83)
AUTHORS Sternsdorf, T., Jensen, K. and Will, H.
TITLE Evidence for covalent modification of the nuclear dot-associated proteins PM1 and Sp100 by PIC1/SUMO-1
JOURNAL J. Cell Biol. 139 (7), 1621-1634 (1997)
MEDLINE 98075076
PUBMED 9412458
REFERENCE 3 (bases 1 to 83)
AUTHORS Guldner, H.H., Szosteck, C. and Will, H.
TITLE Alternative splice variants of Sp100
JOURNAL Unpublished
FEATURES Location/Qualifiers
source 1..83
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2q37"
/tissue_type="placenta"
/note="putative"
/codon_start=1
/product="nuclear autoantigen"
/protein_id="AAI77441.1"
/db_xref="GI:1865390"
/translation="LKKKKKKCHPQPPQGLLEQS"
BASE COUNT 33 a 22 c 17 g 11 t
ORIGIN
Query Match 0.5%; Score 20; DB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2567 TTTCTCTCTCTCTTTT 2586
Db 24 TTTCTCTCTCTTTT 5
RESULT 2
AX165819 50 bp DNA linear PAT 22-JUN-2001
LOCUS AX165819
DEFINITION Sequence 1014 from Patent WO0138586.
ACCESSION AX165819
VERSION AX165819.1 GI:14546648
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 50)
TITLE Shinkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0138586-A 1014 31-MAY-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg4391048"
variation 26
/note="single nucleotide polymorphism"
BASE COUNT 1 a 11 c 2 g 36 t
ORIGIN
Query Match 0.5%; Score 19; DB 6; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2567 TTTCTCTCTCTTTT 2585
Db 8 TTTCTCTCTTTT 26
RESULT 3
AX18541 51 bp DNA linear PAT 11-MAY-2001
LOCUS AX18541
DEFINITION Sequence 3664 from Patent WO0129262.
ACCESSION AX18541
VERSION AX18541.1 GI:14035492
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 51)
TITLE Picoult-Newburg, L. and Pohl, M.
Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3664 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 5 a 15 c 8 g 23 t
ORIGIN
Query Match 0.5%; Score 18; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2567 TTTCTCTCTTTT 2584
Db 34 TTTCTCTCTTTT 51
RESULT 4
AX042894 25 bp DNA linear PAT 23-NOV-2000
LOCUS AX042894
DEFINITION Sequence 460 from Patent WO0065088.
ACCESSION AX042894
VERSION AX042894.1 GI:11341502
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 25)
AUTHORS Ulfendahl, P.J. and Wong, K.C.
Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 460 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="HLA-C Homozygote Primer Sequence"
BASE COUNT 1 a 5 c 2 g 17 t
ORIGIN
Query Match 0.5%; Score 17; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2999 TTTTTCCTCTTC 3015
Db 6 TTTTTCCTCTTC 22
RESULT 5

A93509/c 42 bp DNA linear PAT 22-JAN-2000
LOCUS A93509
DEFINITION Sequence 2 from Patent WO9740163.
ACCESSION A93509
VERSION A93509.1 GI:6741728
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 42)
AUTHORS Colpan, M. and Schorr, J.
TITLE NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
JOURNAL Patent: WO 9740163-A 2 30-OCT-1997;
COLPAN MERIN (DE); SCHORR JOACHIM (DE)
LOCATION/Qualifiers
FEATURES
1..42
source /organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 17 a 9 c 9 g 7 t
ORIGIN

Query Match 0.5%; Score 17; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2562 CCAGCTTCTCTCTCT 2578
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DB 41 CCAGCTTCTCTCTCT 25

RESULT 6 48 bp DNA linear PAT 22-JAN-2000
LOCUS A93513
DEFINITION Sequence 6 from Patent WO9740163.
ACCESSION A93513
VERSION A93513.1 GI:6741732
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 48)
AUTHORS Colpan, M. and Schorr, J.
TITLE NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
JOURNAL Patent: WO 9740163-A 6 30-OCT-1997;
COLPAN MERIN (DE); SCHORR JOACHIM (DE)
LOCATION/Qualifiers
FEATURES
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source /organism="unidentified"
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BASE COUNT 19 a 11 c 9 g 9 t
ORIGIN

Query Match 0.5%; Score 17; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2562 CCAGCTTCTCTCTCT 2578
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DB 47 CCAGCTTCTCTCTCT 31

RESULT 7 48 bp DNA linear PAT 22-JAN-2000
LOCUS A93514
DEFINITION Sequence 7 from Patent WO9740163.
ACCESSION A93514
VERSION A93514.1 GI:6741733
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 48)
AUTHORS Colpan, M. and Schorr, J.

TITLE NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
JOURNAL Patent: WO 9740163-A 7 30-OCT-1997;
COLPAN MERIN (DE); SCHORR JOACHIM (DE)
LOCATION/Qualifiers
FEATURES
1..48
source /organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 8 a 10 c 12 g 18 t
ORIGIN

Query Match 0.5%; Score 17; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2562 CCAGCTTCTCTCTCT 2578
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DB 6 CCAGCTTCTCTCTCT 22

RESULT 8 51 bp DNA linear PAT 11-MAY-2001
LOCUS AX116989/c
DEFINITION Sequence 2112 from Patent WO0129262.
ACCESSION AX116989
VERSION AX116989.1 GI:14033931
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 51)
AUTHORS Picoult-Newbury, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2112 26-APR-2001;
Orchid Biosciences, Inc. (US)
LOCATION/Qualifiers
FEATURES
1..51
source /organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 20 a 9 c 7 g 15 t
ORIGIN

Query Match 0.5%; Score 17; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2577 TTTTCTTTCTGAAA 2593
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DB 19 TTTTCTTTCTGAAA 3

RESULT 9 54 bp DNA linear PAT 13-MAY-1997
LOCUS I38031
DEFINITION Sequence 1044 from patent US 5612215.
ACCESSION I38031
VERSION I38031.1 GI:2086021
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 54)
AUTHORS Draper, K.G., Pavco, P., McSwiggen, J., Gustafson, J. and
Stromelystin targeted ribozymes
TITLE Patent: US 5612215-A 1044 18-MAR-1997;
JOURNAL Location/Qualifiers
FEATURES
1..54
source /organism="unknown"
BASE COUNT 18 a 9 c 18 g 9 t
ORIGIN

Query Match 0.5%; Score 17; DB 6; Length 54;

Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3286 TCAGGGGAGAGGGGG 3302
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Db 1 TCAGGGGAGAGGGGG 17

RESULT 10

LOCUS 194881 54 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 1044 from patent US 5731295.
ACCESSION 194881
VERSION 194881.1 GI:3939351

KEYWORDS
SOURCE Unknown.

REFERENCE 1 (bases 1 to 54)
AUTHORS Draper,K.G., Pavco,P., MCSwigen,J., Gustofson,J. and
Stinchcomb,D.T.

TITLE Method of reducing stromelysin RNA via ribozymes
JOURNAL Patent: US 5731295-A 1044 24-MAR-1998;
FEATURES Location/Qualifiers
source 1..54
/organism="unknown"

BASE COUNT 18 a 9 c 18 g 9 t
ORIGIN

Query Match 0.5%; Score 17; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3286 TCAGGGGAGAGGGGG 3302
|||||
Db 1 TCAGGGGAGAGGGGG 17

RESULT 11
AX482998 65 bp DNA linear PAT 16-AUG-2002
LOCUS
DEFINITION Sequence 298 from Patent WO02053728.
ACCESSION AX482998
VERSION AX482998.1 GI:22317418

KEYWORDS
SOURCE Candida albicans.
ORGANISM Candida albicans

REFERENCE 1
AUTHORS Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 298 11-JUL-2002;
Bilita Pharmaceuticals, Inc. (US)

FEATURES Location/Qualifiers
source 1..65
/organism="Candida albicans"
/db_xref="taxon:5476"

BASE COUNT 17 a 8 c 9 g 31 t
ORIGIN

Query Match 0.5%; Score 17; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2567 TTTCCTCTCTCTTTT 2583
|||||
Db 2 TTTCCTCTCTCTTTT 18

RESULT 12
E25574 24 bp RNA linear PAT 18-JUN-2001
LOCUS

DEFINITION RNA molecule inhibiting hepatitis C virus NS3 protease.
ACCESSION E25574
VERSION E25574.1 GI:13024840
KEYWORDS JP 1999137252-A/6.
SOURCE unidentified.
ORGANISM unidentified

REFERENCE 1 (bases 1 to 24)
AUTHORS Satoshi,N., Pemmeccha,K. and Kotaro,F.
TITLE RNA molecule inhibiting hepatitis C virus NS3 protease
JOURNAL Patent: JP 1999137252-A 6 25-MAY-1999;
AGENCY OF IND SCIENCE & TECHNOL

COMMENT OS Unidentified
PN JP 1999137252-A/6
PD 25-MAY-1999
PR 07-NOV-1997 JP 1997305344

PI SATOSHI NISHIKAWA,PEMMECCHA KUMARU,KOTARO FUKUDA PC
C12N15/09,A61K31/70,A61K31/70,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;

FEATURES Location/Qualifiers
source 1..24
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/db_xref="taxon:32644"

BASE COUNT 0 a 12 c 0 g 12 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2217 TCCTCTCTCTCTTC 2232
|||||
Db 8 TCCTCTCTCTCTTC 23

RESULT 13
E25576 24 bp DNA linear PAT 18-JUN-2001
LOCUS
DEFINITION RNA molecule inhibiting hepatitis C virus NS3 protease.
ACCESSION E25576
VERSION E25576.1 GI:13024842
KEYWORDS JP 1999137252-A/8.
SOURCE unidentified.

ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Satoshi,N., Pemmeccha,K. and Kotaro,F.
TITLE RNA molecule inhibiting hepatitis C virus NS3 protease
JOURNAL Patent: JP 1999137252-A 8 25-MAY-1999;
AGENCY OF IND SCIENCE & TECHNOL

COMMENT OS Unidentified
PN JP 1999137252-A/8
PD 25-MAY-1999
PR 07-NOV-1997 JP 1997305344

PI SATOSHI NISHIKAWA,PEMMECCHA KUMARU,KOTARO FUKUDA PC
C12N15/09,A61K31/70,A61K31/70,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;

FEATURES Location/Qualifiers
source 1..24
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 12 a 0 c 12 g 0 t
ORIGIN

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Job time : 9360 secs

Query Match 0.4%; Score 16; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2217 TCTCTCCTCTCTCTC 2232
 DB 17 TCTCTCCTCTCTCTC 2

RESULT 14

AX042974

LOCUS AX042974 25 bp DNA linear PAT 23-NOV-2000
 DEFINITION Sequence 540 from Patent WO0065088.
 ACCESSION AX042974
 VERSION AX042974.1 GI:11341582
 KEYWORDS

SOURCE

synthetic construct.
 ORGANISM
 artificial sequences.

REFERENCE

1 (bases 1 to 25)
 Ulfendahl, P.J. and Wong, K.C.
 TITLE Primers for identifying typing or classifying nucleic acids
 JOURNAL Patent: WO 0065088-A 540 02-NOV-2000;
 Amersham Pharmacia Biotech AB (SE)
 Location/Qualifiers

FEATURES
 source 1..25
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="16S rRNA Homozygote Primer Sequence"

BASE COUNT 4 a 2 c 5 g 14 t
 ORIGIN

Query Match 0.4%; Score 16; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2577 TTTTCTCTCTGAAA 2592
 DB 3 TTTTCTCTCTGAAA 18

RESULT 15

AX043091

LOCUS AX043091 25 bp DNA linear PAT 23-NOV-2000
 DEFINITION Sequence 657 from Patent WO0065088.
 ACCESSION AX043091
 VERSION AX043091.1 GI:11341699
 KEYWORDS

SOURCE

synthetic construct.
 ORGANISM
 artificial sequences.

REFERENCE

1 (bases 1 to 25)
 Ulfendahl, P.J. and Wong, K.C.
 TITLE Primers for identifying typing or classifying nucleic acids
 JOURNAL Patent: WO 0065088-A 657 02-NOV-2000;
 Amersham Pharmacia Biotech AB (SE)
 Location/Qualifiers

FEATURES
 source 1..25
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="16S rRNA Homozygote Primer Sequence"

BASE COUNT 2 a 5 c 2 g 16 t
 ORIGIN

Query Match 0.4%; Score 16; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 68 TTTTCTCTCAGATG 83
 DB 4 TTTTCTCTCAGATG 19

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